

## BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site  
**Reference:** Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program  Matrix

Parameters used in BLASTN program only:

Reward for a match:  Penalty for a mismatch:

☒ Use Mega BLAST Strand option

Open gap  and extension gap  penalties  
gap x\_dropoff  expect  word size  Filter ☒

Sequence 1 Enter accession or GI  or download from file

or sequence in FASTA format from:  to:

```
cvntprmpnrnfrqgrgaoprcqegsprqssprcgggqggnggggqqkmaigsgvldaaak  
gyvvttnnhvvdnatvikvqlsdgrkfdakmvgkdpdsdialiqnkpnltaikmadsdal  
rvgydtvaignpfglgetvtsgivsalgrsglnaenyenfiqtdaaainrgnsggalvnlng  
eligintailapdggngigfaipsnmvknltsqmveygqvkrgeimgtelnselakam  
kvdaqrqafvsvqlpnssaaakagikagdvitslngkpissfaalraqvgtmpvgskltlgl  
lrdgkqvnvnlelqqssqngvdssisfngiegaemsnkgkdqgvvnnvktgtgtpaaqiglk  
kgdviiganqqavkniaelrkvltdskpsvlnlniqrgdstiylmq
```

DEGP of E.coli

Sequence 2 Enter accession or GI  or download from file

or sequence in FASTA format from:  to:

```
mgikkvctviciivcigirytarvnqgernavsiikakiineegkxpvnlrcytlqm  
kvaerimaghgperfyvvlmsenrnekdydyfnqikdkaerayffylpyglksfnfiptm  
aelkvksmlpkkvriylaslekvsiaaflstypdaeiktfdgtnnliressylggefav  
ngaikrnfarmmvgdwsiaaktrnasdehytifkglknimddgrrkmtylplfdaselkagd  
etggtrvillgspdkemkeisekaaknfniqyvaphprqtyglsgvtalnspsyviedyilr  
eikknphtryeytffsgaaltmkdfpnvhvyaalkpaslpedywlkpvyalfrqadipilt  
fddkn
```

Gilbert  
SEQ ID NO: 4

Comments and suggestions to: [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)  
Credits to: Tatiana Tatusov and Tom Madden



## Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.1 [Aug-1-2001]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**  
x\_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ Align

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Sequence 1 lcl|seq\_1 Length 473

Sequence 2 lcl|seq\_2 Length 371

No significant similarity was found